

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/104,063DATE: 07/06/98  
TIME: 13:58:38

INPUT SET: S27164.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Lee, James  
6 Wood, William I.  
7  
8 (ii) TITLE OF INVENTION: PF4A Receptors  
9  
10 (iii) NUMBER OF SEQUENCES: 6  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: Genentech, Inc.  
14 (B) STREET: 1 DNA Way  
15 (C) CITY: South San Francisco  
16 (D) STATE: California  
17 (E) COUNTRY: USA  
18 (F) ZIP: 94080  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
22 (B) COMPUTER: IBM PC compatible  
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
24 (D) SOFTWARE: WinPatin (Genentech)  
25  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER:  
28 (B) FILING DATE: 24-June-1998  
29 (C) CLASSIFICATION:  
30  
31 (vii) PRIOR APPLICATION DATA:  
32 (A) APPLICATION NUMBER: 08/701265  
33 (B) FILING DATE: 22-AUG-1996  
34  
35 (vii) PRIOR APPLICATION DATA:  
36 (A) APPLICATION NUMBER: 08/664228  
37 (B) FILING DATE: 06-JUN-1996  
38  
39 (vii) PRIOR APPLICATION DATA:  
40 (A) APPLICATION NUMBER: 08/076093  
41 (B) FILING DATE: 11-JUN-1993  
42  
43 (vii) PRIOR APPLICATION DATA:  
44 (A) APPLICATION NUMBER: 07/810782  
45 (B) FILING DATE: 19-DEC-1991  
46

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47 (viii) ATTORNEY/AGENT INFORMATION:  
48 (A) NAME: Love, Richard B.  
49 (B) REGISTRATION NUMBER: 34,659  
50 (C) REFERENCE/DOCKET NUMBER: P0706P2C2  
51  
52 (ix) TELECOMMUNICATION INFORMATION:  
53 (A) TELEPHONE: 415/225-5530  
54 (B) TELEFAX: 415/952-9881  
55 (C) TELEX: 910/371-7168  
56  
57 (2) INFORMATION FOR SEQ ID NO:1:  
58  
59 (i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 1933 base pairs  
61 (B) TYPE: Nucleic Acid  
62 (C) STRANDEDNESS: Single  
63 (D) TOPOLOGY: Linear  
64  
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
66  
67  
68 CCTGGCCGGT GCTTCAGTTA GATCAAACCA TTGCTGAAAC TGAAGAGGAC 50  
69  
70 ATGTCAAATA TTACAGATCC ACAGATGTGG GATTTTGATG ATCTAAATTT 100  
71  
72 CACTGGCATG CCACCTGCAG ATGAAGATTA CAGCCCCTGT ATGCTAGAAA 150  
73  
74 CTGAGACACT CAACAAGTAT GTTGTGATCA TCGCCTATGC CCTAGTGTTT 200  
75  
76 CTGCTGAGCC TGCTGGGAAA CTCCCTGGTG ATGCTGGTCA TCTTATACAG 250  
77  
78 CAGGGTCGGC CGCTCCGTCA CTGATGTCTA CCTGCTGAAC CTGGCCTTGG 300  
79  
80 CCGACCTACT CTTTGCCCTG ACCTTGCCCA TCTGGGCCGC CTCCAAGGTG 350  
81  
82 AATGGCTGGA TTTTGGCAC ATTCCGTGTC AAGGTGGTCT CACTCCTGAA 400  
83  
84 GGAAGTCAAC TTCTACAGTG GCATCCTGCT GTTGGCCTGC ATCAGTGTGG 450  
85  
86 ACCGTTACCT GGCCATTGTC CATGCCACAC GCACACTGAC CCAGAAGCGT 500  
87  
88 CACTTGGTCA AGTTTGTGTTG TCTTGGCTGC TGGGGACTGT CTATGAATCT 550  
89  
90 GTCCCTGCCC TTCTTCCTTT TCCGCCAGGC TTACCATCCA AACAATTCCA 600  
91  
92 GTCCAGTTTG CTATGAGGTC CTGGGAAATG ACACAGCAA ATGGCGGATG 650  
93  
94 GTGTTGCGGA TCCTGCCTCA CACCTTTGGC TTCATCGTGC CGCTGTTTGT 700  
95  
96 CATGCTGTTT TGCTATGGAT TCACCCTGCG TACACTGTTT AAGGCCACA 750  
97  
98 TGGGGCAGAA GCACCGAGCC ATGAGGGTCA TCTTTGCTGT CGTCCTCATC 800  
99

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100 TTCCTGCTTT GCTGGCTGCC CTACAACCTG GTCCTGCTGG CAGACACCCT 850  
101  
102 CATGAGGACC CAGGTGATCC AGGAGACCTG TGAGCGCCGC AACAAATCG 900  
103  
104 GCCGGGCCCT GGATGCCACT GAGATTCTGG GATTCTCTCA TAGCTGCCTC 950  
105  
106 AACCCCATCA TCTACGCCTT CATCGGCCAA AATTTTCGCC ATGGATTCCCT 1000  
107  
108 CAAGATCCTG GCTATGCATG GCCTGGTCAG CAAGGAGTTC TTGGCACGTC 1050  
109  
110 ATCGTGTTAC CTCCTACACT TCTTCGTCTG TCAATGTCTC TTCCAACCTC 1100  
111  
112 TGAAAACCAT CGATGAAGGA ATATCTCTTC TCAGAAGGAA AGAATAACCA 1150  
113  
114 ACACCCTGAG GTTGTGTGTG GAAGGTGATC TGGCTCTGGA CAGGCACTAT 1200  
115  
116 CTGGGTTTTG GGGGGACGCT ATAGGATGTG GGAAGTTAG GAACTGGTGT 1250  
117  
118 CTTCAGGGGC CACACCAACC TTCTGAGGAG CTGTTGAGGT ACCTCCAAGG 1300  
119  
120 ACCGGCCTTT GCACCTCCAT GGAAACGAAG CACCATCATT CCCGTTGAAC 1350  
121  
122 GTCACATCTT TAACCCACTA ACTGGCTAAT TAGCATGGCC ACATCTGAGC 1400  
123  
124 CCCGAATCTG ACATTAGATG AGAGAACAGG GCTGAAGCTG TGTCCTCATG 1450  
125  
126 AGGGCTGGAT GCTCTCGTTG ACCCTCACAG GAGCATCTCC TCAACTCTGA 1500  
127  
128 GTGTTAAGCG TTGAGCCACC AAGCTGGTGG CTCTGTGTGC TCTGATCCGA 1550  
129  
130 GCTCAGGGGG GTGGTTTTCC CATCTCAGGT GTGTTGCAGT GTCTGCTGGA 1600  
131  
132 GACATTGAGG CAGGCACTGC CAAAACATCA ACCTGCCAGC TGGCCTTGTC 1650  
133  
134 AGGAGCTGGA AACACATGTT CCCCTTGGGG GTGGTGGATG AACAAAGAGA 1700  
135  
136 AAGAGGGTTT GGAAGCCAGA TCTATGCCAC AAGAACCCCC TTTACCCCCA 1750  
137  
138 TGACCAACAT CGCAGACACA TGTGCTGGCC ACCTGCTGAG CCCCAAGTGG 1800  
139  
140 AACGAGACAA GCAGCCCTTA GCCCTTCCCC TCTGCAGCTT CCAGGCTGGC 1850  
141  
142 GTGCAGCATC AGCATCCCTA GAAAGCCATG TGCAGCCACC AGTCCATTGG 1900  
143  
144 GCAGGCAGAT GTTCCTAATA AAGCTTCTGT TCC 1933  
145

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/104,063

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153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

154
155 Met Ser Asn Ile Thr Asp Pro Gln Met Trp Asp Phe Asp Asp Leu
156 1 5 10 15
157
158 Asn Phe Thr Gly Met Pro Pro Ala Asp Glu Asp Tyr Ser Pro Cys
159 20 25 30
160
161 Met Leu Glu Thr Glu Thr Leu Asn Lys Tyr Val Val Ile Ile Ala
162 35 40 45
163
164 Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val
165 50 55 60
166
167 Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp
168 65 70 75
169
170 Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu
171 80 85 90
172
173 Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe
174 95 100 105
175
176 Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn
177 110 115 120
178
179 Phe Tyr Ser Gly Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg
180 125 130 135
181
182 Tyr Leu Ala Ile Val His Ala Thr Arg Thr Leu Thr Gln Lys Arg
183 140 145 150
184
185 His Leu Val Lys Phe Val Cys Leu Gly Cys Trp Gly Leu Ser Met
186 155 160 165
187
188 Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg Gln Ala Tyr His Pro
189 170 175 180
190
191 Asn Asn Ser Ser Pro Val Cys Tyr Glu Val Leu Gly Asn Asp Thr
192 185 190 195
193
194 Ala Lys Trp Arg Met Val Leu Arg Ile Leu Pro His Thr Phe Gly
195 200 205 210
196
197 Phe Ile Val Pro Leu Phe Val Met Leu Phe Cys Tyr Gly Phe Thr
198 215 220 225
199
200 Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys His Arg Ala
201 230 235 240
202
203 Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp
204 245 250 255
205

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206	Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr	
207	260	270
208		
209	Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg	
210	275	285
211		
212	Ala Leu Asp Ala Thr Glu Ile Leu Gly Phe Leu His Ser Cys Leu	
213	290	300
214		
215	Asn Pro Ile Ile Tyr Ala Phe Ile Gly Gln Asn Phe Arg His Gly	
216	305	315
217		
218	Phe Leu Lys Ile Leu Ala Met His Gly Leu Val Ser Lys Glu Phe	
219	320	330
220		
221	Leu Ala Arg His Arg Val Thr Ser Tyr Thr Ser Ser Ser Val Asn	
222	335	345
223		
224	Val Ser Ser Asn Leu	
225	350	
226		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

230 (A) LENGTH: 1737 base pairs  
231 (B) TYPE: Nucleic Acid  
232 (C) STRANDEDNESS: Single  
233 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

234  
235  
236  
237  
238 GAATTCAGT GTGCTGGCGG CGCGGCGCAA AGTGACGCCG AGGGCCTGAG 50  
239  
240 TGCTCCAGTA GCCACCGCAT CTGGAGAACC AGCGGTTACC ATGGAGGGGA 100  
241  
242 TCAGTATATA CACTTCAGAT AACTACACCG AGGAAATGGG CTCAGGGGAC 150  
243  
244 TATGACTCCA TGAAGGAACC CTGTTTCCGT GAAGAAAATG CTAATTTCAA 200  
245  
246 TAAAATCTTC CTGCCCACCA TCTACTCCAT CATCTTCTTA ACTGGCATTG 250  
247  
248 TGGGCAATGG ATTGGTCATC CTGGTCATGG GTTACCAGAA GAAACTGAGA 300  
249  
250 AGCATGACGG ACAAGTACAG GCTGCACCTG TCAGTGGCCG ACCTCCTCTT 350  
251  
252 TGTCATCAGC CTTCCCTTCT GGGCAGTTGA TGCCGTGGCA AACTGGTACT 400  
253  
254 TTGGGAACTT CCTATGCAAG GCAGTCCATG TCATCTACAC AGTCAACCTC 450  
255  
256 TACAGCAGTG TCCTCATCCT GGCCTTCATC AGTCTGGACC GCTACCTGGC 500  
257  
258 CATCGTCCAC GCCACCAACA GTCAGAGGCC AAGGAAGCTG TTGGCTGAAA 550

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/104,063**

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*INPUT SET: S27164.raw*

Line

Error

Original Text